

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/773,440
Source: FEWO
Date Processed by STIC: 06/20/2005

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)**
- 2. U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
- 3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

$$10 \overline{) 773,440}$$

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- | | | |
|----|---|---|
| 1 | <p>_____ Wrapped Nucleics
 Wrapped Aminos</p> | <p>The number/text at the end of each line “wrapped” down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent “wrapping.”</p> |
| 2 | <p>_____ Invalid Line Length</p> | <p>The rules require that a line not exceed 72 characters in length. This includes white spaces.</p> |
| 3 | <p>_____ Misaligned Amino
 Numbering</p> | <p>The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.</p> |
| 4 | <p>_____ Non-ASCII</p> | <p>The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.</p> |
| 5 | <p>_____ Variable Length</p> | <p>Sequence(s) _____ contain n’s or Xaa’s representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.</p> |
| 6 | <p>_____ PatentIn 2.0
 “bug”</p> | <p>A “bug” in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.</p> |
| 7 | <p>_____ Skipped Sequences
 (OLD RULES)</p> | <p>Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where “X” is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where “X” is shown)
 This sequence is intentionally skipped</p> <p>Please also adjust the “(ii) NUMBER OF SEQUENCES:” response to include the skipped sequences.</p> |
| 8 | <p>_____ Skipped Sequences
 (NEW RULES)</p> | <p>Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000</p> |
| 9 | <p>_____ Use of n’s or Xaa’s
 (NEW RULES)</p> | <p>Use of n’s and/or Xaa’s have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n’s or Xaa’s are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.</p> |
| 10 | <p>_____ Invalid <213>
 Response</p> | <p>Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence</p> |
| 11 | <p>_____ Use of <220></p> | <p>Sequence(s) _____ missing the <220> “Feature” and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> “Organism” response is “Artificial Sequence” or “Unknown.” Please explain source of genetic material in <220> to <223> section.
 (See “Federal Register,” 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)</p> |
| 12 | <p>_____ PatentIn 2.0
 “bug”</p> | <p>Please do not use “Copy to Disk” function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use “File Manager” or any other manual means to copy file to floppy disk.</p> |
| 13 | <p>_____ Misuse of n/Xaa</p> | <p>“n” can only represent a single nucleotide; “Xaa” can only represent a single amino acid</p> |



IFWO

RAW SEQUENCE LISTING

DATE: 06/20/2005

PATENT APPLICATION: US/10/773,440

TIME: 09:51:42

Input Set : A:\Sequence Listing ASCII, Docket No. 1619.0180001.ST25.txt

Output Set: N:\CRF4\06202005\J773440.raw

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3 <110> APPLICANT: Fradet, Yves
4     Chypre, Camille
5     Piche, Lyson
6     Garon, Genevieve
8 <120> TITLE OF INVENTION: METHOD TO DETECT PROSTATE CANCER IN A SAMPLE
10 <130> FILE REFERENCE: 1619.0180001/JAG/CMB
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/773,440
C--> 12 <141> CURRENT FILING DATE: 2004-02-09
12 <150> PRIOR APPLICATION NUMBER: US 60/445,436
13 <151> PRIOR FILING DATE: 2003-02-07
15 <160> NUMBER OF SEQ ID NOS: 13
17 <170> SOFTWARE: PatentIn version 3.2
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 47
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
24 <400> SEQUENCE: 1
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28 <210> SEQ ID NO: 2
29 <211> LENGTH: 20
30 <212> TYPE: DNA
31 <213> ORGANISM: Homo sapiens
33 <400> SEQUENCE: 2
34 agcattccca accctggcag          20
37 <210> SEQ ID NO: 3
38 <211> LENGTH: 45
39 <212> TYPE: DNA
40 <213> ORGANISM: Homo sapiens
42 <400> SEQUENCE: 3
43 aattctaata cgactcacta tagggcctgc ccataccttta aggaa          45
46 <210> SEQ ID NO: 4
47 <211> LENGTH: 20
48 <212> TYPE: DNA
49 <213> ORGANISM: Homo sapiens
51 <400> SEQUENCE: 4
52 caggaagcac aaaaggaagc          20
55 <210> SEQ ID NO: 5
56 <211> LENGTH: 26
57 <212> TYPE: DNA
58 <213> ORGANISM: Homo sapiens
61 <220> FEATURE:
62 <221> NAME/KEY: misc_feature
63 <222> LOCATION: (1)..(1)

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Does Not Comply
Corrected Diskette Needed

(Pg-2)

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Input Set : A:\Sequence Listing ASCII, Docket No. 1619.0180001.ST25.txt

Output Set: N:\CRF4\06202005\J773440.raw

64 <223> OTHER INFORMATION: n = ROX → Invalid Response
 66 <220> FEATURE:
 67 <221> NAME/KEY: misc_feature
 68 <222> LOCATION: (26)..(26)
 69 <223> OTHER INFORMATION: n = DABCYL → Same Error
 71 <400> SEQUENCE: 5

W--> 72 nccccgtctg cgccggtgtt ctgggn
 75 <210> SEQ ID NO: 6
 76 <211> LENGTH: 30
 77 <212> TYPE: DNA
 78 <213> ORGANISM: Homo sapiens
 81 <220> FEATURE:
 82 <221> NAME/KEY: misc_feature
 83 <222> LOCATION: (1)..(1)
 84 <223> OTHER INFORMATION: n = FAM → Same Error
 86 <220> FEATURE:
 87 <221> NAME/KEY: misc_feature
 88 <222> LOCATION: (30)..(30)
 89 <223> OTHER INFORMATION: n = DABCYL
 91 <400> SEQUENCE: 6

W--> 92 ncgcttgta gggaggaca ttagaagcgn
 95 <210> SEQ ID NO: 7
 96 <211> LENGTH: 506
 97 <212> TYPE: DNA
 98 <213> ORGANISM: Homo sapiens
 100 <400> SEQUENCE: 7

101 caggaagcac aaaaggaagc acagaggtaa gtgctttata aagcactcaa tttctactca	60
103 gaaatttttg atggccttaa gttcctctac tcgtttctat ccttcctact cactgtcctc	120
105 ccggaatcca ctaccgattt tctatttctt gcctcgtatt gtctgactgg ctcaattgga	180
107 tttatcctca cggagtctgg attttctacc cgggctcacc tccgtccctc catatttgtc	240
109 ctccactttc acagatccct gggagaaatg cccggccgcc atcttgggtc atcgatgagc	300
111 ctgcacctgt gcttggtccc gcttggtgagg gaaggacatt agaaaatgaa ttgatgtgtt	360
113 ccttaaagga tgggcaggaa aacagatcct gttgtggata tttatttgaa cgggattaca	420
115 gatttgaaat gaagtcacca aagtgagcat taccaatgag aggaaaacag acgagaaaaa	480
117 cttgatggct tcacaagaca tgcaac	506
120 <210> SEQ ID NO: 8	
121 <211> LENGTH: 278	
122 <212> TYPE: DNA	
123 <213> ORGANISM: Homo sapiens	
125 <400> SEQUENCE: 8	
126 caggaagcac aaaaggaagc acagagatcc ctgggagaaa tgcccggccg ccatcttggg	60
128 tcatcgatga gcctgcctt gtgcctggtc ccgcttgta gggaggaca ttagaaaatg	120
130 aattgatgtg ttctttaaag gatgggcagg aaaacagatc ctgttggtga tatttatttg	180
132 aacgggatta cagatttgaa atgaagtcac caaagtgagc attaccaatg agaggaaaac	240
134 agacgagaaa atcttgatgg cttcacaaga catgcaac	278
137 <210> SEQ ID NO: 9	
138 <211> LENGTH: 2036	
139 <212> TYPE: DNA	
140 <213> ORGANISM: Homo sapiens	

"n" can only represent a single Nucleotide to see Item # 13 of Error Summary Sheet

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

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Input Set : A:\Sequence Listing ASCII, Docket No. 1619.0180001.ST25.txt

Output Set: N:\CRF4\06202005\J773440.raw

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143 <220> FEATURE:
144 <221> NAME/KEY: misc_feature
145 <222> LOCATION: (1472)..(1472) ✓
146 <223> OTHER INFORMATION: n is a, c, g, or t
148 <220> FEATURE:
149 <221> NAME/KEY: misc_feature
150 <222> LOCATION: (1517)..(1517) ✓
151 <223> OTHER INFORMATION: n is a, c, g, or t
153 <220> FEATURE:
154 <221> NAME/KEY: misc_feature ✓
155 <222> LOCATION: (1563)..(1563) ✓
156 <223> OTHER INFORMATION: n is a, c, g, or t
158 <400> SEQUENCE: 9
159 agaagctggc atcagaaaaa cagaggggag atttgtgtgg ctgcagccga gggagaccag 60
161 gaagatctgc atggtgggaa ggacctgatg atacagagga attacaacac atatacttag 120
163 tgtttcaatg aacaccaaga taaataagtg aagagctagt ccgctgtgag tctcctcagt 180
165 gacacagggc tggatcacca tcgacggcac tttctgagta ctgagtgcag caaagaaaga 240
167 ctacagacat ctcaatggca ggggtgagaa ataagaaagg ctgctgactt taccatctga 300
169 ggccacacat ctgctgaaat ggagataatt aacatcacta gaaacagcaa gatgacaata 360
171 taatgtctaa gtagtgacat gtttttgcac atttccagcc cctttaaata tccacacaca 420
173 caggaagcac aaaaggaagc acagagatcc ctgggagaaa tgcccggccg ccatcttggg 480
175 tcatcgatga gcctcgccct gtgcctggtc ccgcttgtga gggaaggaca ttagaaaatg 540
177 aattgatgtg ttccttaaag gatgggcagg aaaacagatc ctgttgtgga tattttattt 600
179 aacgggatta cagatttgaa atgaagtcac aaagtgcagc ttaccaatga gaggaaaaca 660
181 gacgagaaaa tcttgatggc ttcacaagac atgcaacaaa caaaatggaa tactgtgatg 720
183 acatgaggca gccaaagctg ggaggagata accacggggc agagggtcag gattctggcc 780
185 ctgctgccta aactgtgcgt tcataaccaa atcatttcat atttctaacc ctcaaaacaa 840
187 agctgttgta atatctgatc tctacggttc cttctgggcc caacattctc catatatcca 900
189 gccacactca tttttaatat ttagttccca gatctgtact gtgaccttc tacactgtag 960
191 aataacatta ctcattttgt tcaaagacct ttcgtgttgc tgcctaatat gtagctgact 1020
193 gtttttccta aggagtgttc tggcccaggg gatctgtgaa caggctggga agcatctcaa 1080
195 gatctttcca gggttatact tactagcaca cagcatgatc attacggagt gaattatcta 1140
197 atcaacatca tctcagtggt ctttgcccat actgaaattc atttcccact tttgtgcca 1200
199 ttctcaagac ctcaaaatgt cattccatta atatcacagg attaaacttt ttttttaacc 1260
201 tggaagaatt caatgttaca tgcagctatg ggaatttaat tacatatatt gttttccagt 1320
203 gcaaagatga ctaagtcctt tatccctccc ctttgtttga ttttttttcc agtataaagt 1380
205 taaaatgctt agcctgttac tgaggctgta tacagcacag cctctcccca tccctccagc 1440
W--> 207 cttatctgtc atcaccatca acccctccca tnysacctaa acaaaatcta acttgtaatt 1500
209 ccttgaacat gtcaggncat acatttrttc ttctgcctga gaagctcttc cttgtctctt 1560
211 aantctagaa tgatgtaaag ttttgaataa gttgactatc ttacttcatg caaagaaggg 1620
213 acacatatga gattcatcat ccatgagaca gcaaatacta aaagtgtaat ttgattataa 1680
215 gagtttagat aaatatatga aatgcaagak ccacagaggg aatgtttatg gggcacgttt 1740
217 gtaagcctgg gatgtgaagm aaaggcaggg aacctcatag tatcttatat aatatacttc 1800
219 atttctctat ctctatcaca atatccaaca agcttttcac agaattcatg cagtgc aaat 1860
221 ccccaaaggc aacctttatc catttcatgg tgagtgcgct ttagaatttt ggcaaatcat 1920
223 actggtcact tatctcaact ttgagatgtg tttgtccttg tagttaattg aaagaaatag 1980
225 ggcactcttg tgagccactt taggggttcac tcctggcaat aaagaattta caaaga 2036
228 <210> SEQ ID NO: 10
229 <211> LENGTH: 3582

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Output Set: N:\CRF4\06202005\J773440.raw

230 <212> TYPE: DNA

231 <213> ORGANISM: Homo sapiens

233 <400> SEQUENCE: 10

234	acagaagaaa	tagcaagctg	cgagaagctg	gcatcagaaa	aacagagggg	agatttgtgt	60
236	ggctgcagcc	gagggagacc	aggaagatct	gcatgggtgg	aaggacctga	tgatacagag	120
238	gaattacaac	acataacttt	agtgtttcaa	tgaacaccaa	gataaataag	tgaagagcta	180
240	gtccgctgtg	agtctcctca	gtgacacagg	gctggatcac	catcgacggc	actttctgag	240
242	tactcagctg	agcaaagaaa	gactacagac	atctcaatgg	caggggtgag	aaataagaaa	300
244	ggctgctgac	tttaccatct	gaggccacac	atctgctgaa	atggagataa	ttaacatcac	360
246	tagaaacagc	aagatgacaa	tataatgtct	aagtagtgac	atgtttttgc	acatttccag	420
248	cccctttaaa	tatccacaca	cacaggaagc	acaaaaggaa	gcacagagat	ccctgggaga	480
250	aatgcccggc	cgccatcttg	ggcatcgcg	gagcctcgcc	ctgtgcctgg	tcccgttgt	540
252	gagggagga	cattagaaaa	tgaattgatg	tgttccttaa	aggatgggca	ggaaaacaga	600
254	tcctgttgtg	gatatttatt	tgaacgggat	tacagatttg	aaatgaagtc	acaaagtgag	660
256	cattaccaat	gagaggaaaa	cagacgagaa	aatcttgatg	gcttcacaag	acatgcaaca	720
258	aacaaaatgg	aatactgtga	tgacatgagg	cagccaagct	ggggaggaga	taaccacggg	780
260	gcagagggtc	aggattctgg	ccctgctgcc	taaactgtgc	gttcataacc	aatcattttc	840
262	atattttctaa	ccctcaaaac	aaagctgttg	taatatctga	tctctacggg	tccttctggg	900
264	cccaacattc	tccatataat	cagccacact	catttttaat	atttagttcc	cagatctgta	960
266	ctgtgacctt	tctacactgt	agaataacat	tactcatttt	gttcaaagac	ccttcgtgtt	1020
268	gctgcctaata	atgtagctga	ctgtttttcc	taaggagtgt	tctggcccag	gggactgtgt	1080
270	aacaggctgg	gaagcatctc	aagatctttc	cagggttata	cttactagca	cacagcatga	1140
272	tcattacgga	gtgaattatc	taatcaacat	catcctcagt	gtctttgccc	atactgaaat	1200
274	tcattttccca	cttttgtgcc	catttctcaag	acctcaaaat	gtcattccat	taatatcaca	1260
276	ggattaactt	tttttttttaa	cctggaagaa	ttcaatgtta	catgcagcta	tgggaattta	1320
278	attacataatt	ttgtttttcca	gtgcaaagat	gactaagtcc	tttatccctc	ccctttgttt	1380
280	gattttttttt	ccagtataaaa	gttaaaatgc	ttagccttgt	actgaggctg	tatacagcac	1440
282	agcctctccc	catccctcca	gccttatctg	tcatcaccat	caaccctcc	cataccacct	1500
284	aaacaaaatc	taacttgtaa	ttccttgaac	atgtcaggac	atacattatt	ccttctgcct	1560
286	gagaagctct	tccttgtctc	ttaaactctag	aatgatgtaa	agttttgaat	aagttgacta	1620
288	tcttacttca	tgcaaagaag	ggacacatat	gagattcatc	atcacatgag	acagcaaata	1680
290	ctaaaagtgt	aatttgatta	taagagttta	gataaatata	tgaaatgcaa	gagccacaga	1740
292	gggaatgttt	atggggcacg	tttghtaagcc	tgggatgtga	agcaaaggca	gggaacctca	1800
294	tagtatctta	tataatatac	ttcattttctc	tatctctatc	acaatatcca	acaagctttt	1860
296	cacagaattc	atgcagtgca	aatccccaaa	ggtaaccttt	atccatttca	tgggtagtg	1920
298	gctttagaat	tttggcaaat	catactgggc	acttatctca	actttgagat	gtgtttgtcc	1980
300	ttgtagttaa	ttgaaagaaa	tagggcactc	ttgtgagcca	ctttagggtt	cactcctggc	2040
302	aataaagaat	ttacaaagag	ctactcagga	ccagttgtta	agagctctgt	gtgtgtgtgt	2100
304	gtgtgtgtgt	gagtgtacat	gccaaagtgt	gcctctctct	cttgacccat	tatttcagac	2160
306	ttaaaacaag	catgttttca	aatggcacta	tgagctgcca	atgatgtatc	accaccatat	2220
308	ctcattattc	tccagtaaat	gtgataataa	tgtcatctgt	taacataaaa	aaagtttgac	2280
310	ttcacaaaag	cagctggaaa	tggacaacca	caatatgcat	aaatctaact	cctaccatca	2340
312	gctacacact	gcttgacata	tattgttaga	agcacctcgc	atttgtgggt	tctcttaagc	2400
314	aaaataactg	cattaggtct	cagctggggc	tgtgcatcag	gcggtttgag	aaatattcaa	2460
316	ttctcagcag	aagccagaat	ttgaattccc	tcactcttta	ggaatcattt	accaggtttg	2520
318	gagaggattc	agacagctca	gggtgctttca	ctaagtgtct	tgaacttctg	tccctctttg	2580
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322	taagaactct	gagtgatatc	aacattaggg	attcaaagaa	atattagatt	taagctcaca	2700
324	ctggtcaaaa	ggaaccaaga	tacaaagaac	tctgagctgt	catcgtcccc	atctctgtga	2760

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Input Set : A:\Sequence Listing ASCII, Docket No. 1619.0180001.ST25.txt

Output Set: N:\CRF4\06202005\J773440.raw

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326 gccacaacca acagcaggac ccaacgcatg tctgagatcc ttaaatacaag gaaaccagtg 2820
328 tcatgagttg aattctccta ttatggatgc tagcttctgg ccattctctg ctctcctctt 2880
330 gacacatatt agcttctagc ctttgcttcc acgactttta tcttttctcc aacacatcgc 2940
332 ttaccaatcc tctctctgct ctgttgcttt ggacttcccc acaagaattt caacgactct 3000
334 caagtctttt cttccatccc caccactaac ctgaattgcc tagaccctta tttttattaa 3060
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348 ctacatttga gaattccaat taggaactca catgttttat ctgccctatc aattttttaa 3480
350 acttgctgaa aattaagttt tttcaaaatc tgtccttgta aattactttt tcttacagtg 3540
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356 <211> LENGTH: 7130
357 <212> TYPE: DNA
358 <213> ORGANISM: Homo sapiens
360 <400> SEQUENCE: 11
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365 tatctgtgga gctggattct gggttgggag tgcaaggaaa agaattgtact aaatgccaag 180
367 acatctattt caggagcatg aggaataaaa gttctagttt ctggtctcag agtgggtcag 240
369 ggatcaggga gtctcacaat ctctgagtgt ctggtgtctt agggcacact gggctctgga 300
371 gtgcaaagga tctaggcacg tgaggctttg tatgaagaat cggggatcgt acccaccccc 360
373 tgtttctgtt tcatcctggg catgtctcct ctgcctttgt cccctagatg aagtctccat 420
375 gagctacaag ggctgtgtgc atccagggtg atctagtaat tgcagaacag caagtgtctag 480
377 ctctccctcc ccttccacag ctctgggtgt gggagggggg tgtccagcct ccagcagcat 540
379 ggggagggcc ttggtcagcc tctgggtgcc agcagggcag gggcggagtc ctggggaatg 600
381 aaggttttat agggctcctg ggggaggctc cccagcccca agcttaccac ctgcaccggg 660
383 agagctgtgt caccatgtgg gtcccggttg tcttcctcac cctgtccgtg acgtggattg 720
385 gtgagagggg ccattggttg ggggatgcag gagagggagc cagccctgac tgtcaagctg 780
387 aggtcttttc cccccaacc cagcacccca gccagacag ggagctgggc tcttttctgt 840
389 ctctcccagc cccacttcaa gccataccc ccagccctc catattgcaa cagtctcac 900
391 tcccacacca ggtccccgt cctcccact taccacagaa ctttctcccc attgccagc 960
393 cagctccctg ctcccagctg ctttactaaa ggggaagttc ctgggcatct ccgtgtttct 1020
395 ctttgtgggg ctcaaaacct ccaaggacct ctctcaatgc cattggttcc ttggaccgta 1080
397 tcaactggtc atctcctgag cccctcaatc ctatcacagt ctactgactt ttccattca 1140
399 gctgtgagtg tccaacccta tcccagagac cttgatgctt ggccctccaa tcttgcccta 1200
401 ggataccag atgccaacca gacacctcct tcttcctagc caggctatct ggccctgagc 1260
403 aacaaatggg tccctcagtc tggcaatggg actctgagaa ctctcattc cctgactctt 1320
405 agccccagac tcttcattca gtggcccaca ttttcttag gaaaaacatg agcatcccca 1380
407 gccacaactg ccagctctct gattcccca atctgcatcc ttttcaaaac ctaaaaacaa 1440
409 aaagaaaaac aaataaaaca aaaccaactc agaccagaac tgttttctca acctgggact 1500
411 tcctaaactt tccaaaacct tcctcttcca gcaactgaac ctggccataa ggcacttatc 1560
413 cctgggttct agcaccctt atcccctcag aatccacaac ttgtaccaag tttcccttct 1620
415 ccagctccaa gaccccaaat caccacaaag gacccaatcc ccagactcaa gatatggtct 1680
417 gggcgctgtc ttgtgtctcc taccctgatc cctgggttca actctgctcc cagagcatga 1740
419 agcctctcca ccagcaccag ccaccaacct gcaaacctag ggaagattga cagaattccc 1800

```

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/773,440

DATE: 06/20/2005
TIME: 09:51:43

Input Set : A:\Sequence Listing ASCII, Docket No. 1619.0180001.ST25.txt
Output Set: N:\CRF4\06202005\J773440.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 1, 26

Seq#:6; N Pos. 1, 30

Seq#:9; N Pos. 1472, 1517, 1563

VERIFICATION SUMMARY

DATE: 06/20/2005

PATENT APPLICATION: US/10/773,440

TIME: 09:51:43

Input Set : A:\Sequence Listing ASCII, Docket No. 1619.0180001.ST25.txt

Output Set: N:\CRF4\06202005\J773440.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:72 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:92 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:207 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:1440
M:341 Repeated in SeqNo=9